

## SEQUENCE LISTING

<110> Pohl, Jens  
Bechtold, Rolf  
Kruse, Michael

<120> Osteoinductive Materials

<130> 2923-725

<140> US 10/550,958  
<141> 2005-09-28

<150> PCT/EP04/003238

<151> 2004-03-26

<160> 5

<170> PatentIn version 3.5

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<212> DNA  
<213> Homo sapiens

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<222> (640)..(2142)

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ttcctgagtt cagggttgta aaagattttt ctgagcacct gcaggcctgt gagtgtgtgt 180

gtgtgtgtgt gtgtgtgtgt gtgtgtgtga agtattttca ctggaaagga ttcaaaaacta 240

ggggggaaaa aaaaactgga gcacacagggc agcattacgc catttttcct tcttggaaaa 300

tccctcagcc ttataacaagc ctccttcaag ccctcagtca gttgtgcagg agaaaggggg 360

cgggtggctt tctcctttca agaacgagtt atttcagct gctgactgga gacgggtgcac 420

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cgctgttctc tttgggtgtca ttcagcggct ggccagagg atg aga ctc ccc aaa Met Arg Leu Pro Lys 1 5	654
ctc ctc act ttc ttg ctt tgg tac ctg gct tgg ctg gac ctg gaa ttc Leu Leu Thr Phe Leu Leu Trp Tyr Leu Ala Trp Leu Asp Leu Glu Phe 10 15 20	702
atc tgc act gtg ttg ggt gcc cct gac ttg ggc cag aga ccc cag ggg Ile Cys Thr Val Leu Gly Ala Pro Asp Leu Gly Gln Arg Pro Gln Gly 25 30 35	750
acc agg cca gga ttg gcc aaa gca gag gcc aag gag agg ccc ccc ctg Thr Arg Pro Gly Leu Ala Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu 40 45 50	798
gcc cgAAC gtc ttc agg cca ggg ggt cac agc tat ggt ggg ggg gcc Ala Arg Asn Val Phe Arg Pro Gly Gly His Ser Tyr Gly Gly Ala 55 60 65	846
acc aat gcc aat gcc agg gca aag gga ggc acc ggg cag aca gga ggc Thr Asn Ala Asn Ala Arg Ala Lys Gly Gly Thr Gly Gln Thr Gly Gly 70 75 80 85	894
ctg aca cag ccc aag aag gat gaa ccc aaa aag ctg ccc ccc aga ccg Leu Thr Gln Pro Lys Lys Asp Glu Pro Lys Lys Leu Pro Pro Arg Pro 90 95 100	942
ggc ggc cct gaa ccc aag cca gga cac cct ccc caa aca agg cag gct Gly Gly Pro Glu Pro Lys Pro Gly His Pro Pro Gln Thr Arg Gln Ala 105 110 115	990
aca gcc cgAAC act gtg acc cca aaa gga cag ctt ccc gga ggc aag gca Thr Ala Arg Thr Val Thr Pro Lys Gly Gln Leu Pro Gly Gly Lys Ala 120 125 130	1038
ccc cca aaa gca gga tct gtc ccc agc tcc ttc ctg ctg aag aag gcc Pro Pro Lys Ala Gly Ser Val Pro Ser Ser Phe Leu Leu Lys Lys Ala 135 140 145	1086
agg gag ccc ggg ccc cca cga gag ccc aag gag ccg ttt cgc cca ccc Arg Glu Pro Gly Pro Pro Arg Glu Pro Lys Glu Pro Phe Arg Pro Pro 150 155 160 165	1134
ccc atc aca ccc cac gag tac atg ctc tcg ctg tac agg acg ctg tcc Pro Ile Thr Pro His Glu Tyr Met Leu Ser Leu Tyr Arg Thr Leu Ser 170 175 180	1182
gat gct gac aga aag gga ggc aac agc agc gtg aag ttg gag gct ggc Asp Ala Asp Arg Lys Gly Gly Asn Ser Ser Val Lys Leu Glu Ala Gly 185 190 195	1230
ctg gcc aac acc atc acc agc ttt att gac aaa ggg caa gat gac cga Leu Ala Asn Thr Ile Thr Ser Phe Ile Asp Lys Gly Gln Asp Asp Arg	1278

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ggt ccc gtg gtc agg aag cag agg tac gtg ttt gac att agt gcc ctg Gly Pro Val Val Arg Lys Gln Arg Tyr Val Phe Asp Ile Ser Ala Leu 215	220	225	1326
gag aag gat ggg ctg ctg ggg gcc gag ctg cg <sup>g</sup> atc ttg cg <sup>g</sup> aag aag Glu Lys Asp Gly Leu Leu Gly Ala Glu Leu Arg Ile Leu Arg Lys Lys 230	235	240	1374
ccc tcg gac acg gcc aag cca gc <sup>g</sup> gcc ccc gga ggc ggg cg <sup>g</sup> gct gcc Pro Ser Asp Thr Ala Lys Pro Ala Ala Pro Gly Gly Gly Arg Ala Ala 250	255	260	1422
cag ctg aag ctg tcc agc tgc ccc agc ggc cg <sup>g</sup> cag cc <sup>g</sup> gcc tcc ttg Gln Leu Lys Leu Ser Ser Cys Pro Ser Gly Arg Gln Pro Ala Ser Leu 265	270	275	1470
ctg gat gtg cgc tcc gtg cca ggc ctg gac gga tct ggc tgg gag gtg Leu Asp Val Arg Ser Val Pro Gly Leu Asp Gly Ser Gly Trp Glu Val 280	285	290	1518
ttc gac atc tgg aag ctc ttc cga aac ttt aag aac tcg gcc cag ctg Phe Asp Ile Trp Lys Leu Phe Arg Asn Phe Lys Asn Ser Ala Gln Leu 295	300	305	1566
tgc ctg gag ctg gag gcc tgg gaa cg <sup>g</sup> ggc agg gcc gtg gac ctc cgt Cys Leu Glu Leu Glu Ala Trp Glu Arg Gly Arg Ala Val Asp Leu Arg 310	315	320	1614
ggc ctg ggc ttc gac cgc gcc ccc cg <sup>g</sup> cag gtc cac gag aag gcc ctg Gly Leu Gly Phe Asp Arg Ala Ala Arg Gln Val His Glu Lys Ala Leu 330	335	340	1662
ttc ctg gtg ttt ggc cgc acc aag aaa cg <sup>g</sup> gac ctg ttc ttt aat gag Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp Leu Phe Phe Asn Glu 345	350	355	1710
att aag gcc cgc tct ggc cag gac gat aag acc gtg tat gag tac ctg Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr Val Tyr Glu Tyr Leu 360	365	370	1758
ttc agc cag cg <sup>g</sup> cga aaa cg <sup>g</sup> cg <sup>g</sup> gcc cca ctg gcc act cgc cag ggc Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu Ala Thr Arg Gln Gly 375	380	385	1806
aag cga ccc agc aag aac ctt aag gct cgc tgc agt cg <sup>g</sup> aag gca ctg Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu 390	395	400	1854
cat gtc aac ttc aag gac atg ggc tgg gac gac tgg atc atc gca ccc His Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile Ile Ala Pro 410	415	420	1902
ctt gag tac gag gct ttc cac tgc gag ggg ctg tgc gag ttc cca ttg			1950

Leu	Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu	Gly	Leu	Cys	Glu	Phe	Pro	Leu	
425								430							435	
cgc	tcc	cac	ctg	gag	ccc	acg	aat	cat	gca	gtc	atc	cag	acc	ctg	atg	1998
Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Val	Ile	Gln	Thr	Leu	Met	
440								445							450	
aac	tcc	atg	gac	ccc	gag	tcc	aca	cca	ccc	acc	nnn	tgt	gtg	ccc	acg	2046
Asn	Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro	Pro	Thr	Xaa	Cys	Val	Pro	Thr	
455								460							465	
cgg	ctg	agt	ccc	atc	agc	atc	ctc	ttc	att	gac	tct	gcc	aac	aac	gtg	2094
Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe	Ile	Asp	Ser	Ala	Asn	Asn	Val	
470								475							485	
gtg	tat	aag	cag	tat	gag	gac	atg	gtc	gtg	gag	tcg	tgt	ggc	tgc	agg	2142
Val	Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val	Glu	Ser	Cys	Gly	Cys	Arg	
490								495							500	
tagcagcact	ggccctctgt	cttcctgggt	ggcacatccc	aagagcccct	tcctgcactc											2202
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ctgtccctgg	gacagttgag	aagctgactg	ggcaagagtg	ggagagaaga	ggagagggct											2622
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 <213> Homo sapiens

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Met Arg Leu Pro Lys Leu Leu Thr Phe Leu Leu Trp Tyr Leu Ala Trp

1 5 10 15

Leu Asp Leu Glu Phe Ile Cys Thr Val Leu Gly Ala Pro Asp Leu Gly  
20 25 30

Gln Arg Pro Gln Gly Thr Arg Pro Gly Leu Ala Lys Ala Glu Ala Lys  
35 40 45

Glu Arg Pro Pro Leu Ala Arg Asn Val Phe Arg Pro Gly Gly His Ser  
50 55 60

Tyr Gly Gly Gly Ala Thr Asn Ala Asn Ala Arg Ala Lys Gly Gly Thr  
65 70 75 80

Gly Gln Thr Gly Gly Leu Thr Gln Pro Lys Lys Asp Glu Pro Lys Lys  
85 90 95

Leu Pro Pro Arg Pro Gly Gly Pro Glu Pro Lys Pro Gly His Pro Pro  
100 105 110

Gln Thr Arg Gln Ala Thr Ala Arg Thr Val Thr Pro Lys Gly Gln Leu  
115 120 125

Pro Gly Gly Lys Ala Pro Pro Lys Ala Gly Ser Val Pro Ser Ser Phe  
130 135 140

Leu Leu Lys Lys Ala Arg Glu Pro Gly Pro Pro Arg Glu Pro Lys Glu  
145 150 155 160

Pro Phe Arg Pro Pro Pro Ile Thr Pro His Glu Tyr Met Leu Ser Leu  
165 170 175

Tyr Arg Thr Leu Ser Asp Ala Asp Arg Lys Gly Gly Asn Ser Ser Val  
180 185 190

Lys Leu Glu Ala Gly Leu Ala Asn Thr Ile Thr Ser Phe Ile Asp Lys  
195 200 205

Gly Gln Asp Asp Arg Gly Pro Val Val Arg Lys Gln Arg Tyr Val Phe  
210 215 220

Asp Ile Ser Ala Leu Glu Lys Asp Gly Leu Leu Gly Ala Glu Leu Arg  
225 230 235 240

Ile Leu Arg Lys Lys Pro Ser Asp Thr Ala Lys Pro Ala Ala Pro Gly  
245 250 255

Gly Gly Arg Ala Ala Gln Leu Lys Leu Ser Ser Cys Pro Ser Gly Arg  
260 265 270

Gln Pro Ala Ser Leu Leu Asp Val Arg Ser Val Pro Gly Leu Asp Gly  
275 280 285

Ser Gly Trp Glu Val Phe Asp Ile Trp Lys Leu Phe Arg Asn Phe Lys  
290 295 300

Asn Ser Ala Gln Leu Cys Leu Glu Leu Glu Ala Trp Glu Arg Gly Arg  
305 310 315 320

Ala Val Asp Leu Arg Gly Leu Gly Phe Asp Arg Ala Ala Arg Gln Val  
325 330 335

His Glu Lys Ala Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp  
340 345 350

Leu Phe Phe Asn Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr  
355 360 365

Val Tyr Glu Tyr Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu  
370 375 380

Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys  
385 390 395 400

Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp  
405 410 415

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu  
420 425 430

Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val  
435 440 445

Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr  
450 455 460

Xaa Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp  
465 470 475 480

Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu  
485 490 495

Ser Cys Gly Cys Arg  
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<223> consensus sequence

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<222> (5)..(7)  
<223> Xaa=Y with Y=any amino acid including cysteine

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<222> (10)..(10)  
<223> Xaa=X wtih X=any amino acid except cysteine

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Cys Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Cys  
1 5 10 15

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<221> REPEAT

<222> (8)..(8)

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<221> VARIANT

<222> (9)..(9)

<223> Xaa=X with X=any amino acid except cysteine

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<221> REPEAT

<222> (11)..(11)

<223> Xaa=(Y)31 with Y=any amino acid including cysteine

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<222> (13)..(13)

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Cys Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Cys  
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<211> 13

<212> PRT

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<223> consensus sequence

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<222> (4)..(6)

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<220>

<221> REPEAT

<222> (8)..(8)

<223> Xaa=(X) 31-33 with X=any amino acid except cysteine

<220>

<221> REPEAT

<222> (10)..(10)

<223> Xaa=(X) 31 with X=any amino acid except cysteine

<220>

<221> VARIANT

<222> (12)..(12)

<223> Xaa=X with X=any amino acid except cysteine

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